



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: DIXIT, VISHVA M.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING FAS-ASSOCIATED APOPTOSIS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Morrison & Foerster
  - (B) STREET: 755 Page Mill Road
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/443,982
  - (B) FILING DATE: 18-MAY-1995
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Konski, Antoinette F.
  - (B) REGISTRATION NUMBER: 34,202
  - (C) REFERENCE/DOCKET NUMBER: 20344-21070.20
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 813-5600
  - (B) TELEFAX: (415) 494-0792
  - (C) TELEX: 706141 MRSNFOERS SFO

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1642 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 130..756
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 4..6
  - (D) OTHER INFORMATION: /note= "An in-frame stop codon 130 base pairs upstream of the initiator methionine"
- (ix) FEATURE:
  - (A) NAME/KEY: polyA\_signal
  - (B) LOCATION: 1636..1641
  - (D) OTHER INFORMATION: /note= "Potential poly(A) adenylation signal"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 198..753
- (D) OTHER INFORMATION: /note= "Clone-15, 5' end of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 249..753
- (D) OTHER INFORMATION: /note= "Clone-8, 5' end of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 177..658
- (D) OTHER INFORMATION: /note= "Death Domain of FADD"

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(490..492, "")
- (D) OTHER INFORMATION: /note= "For FADDmt, the sequence is altered to either AAT or AAC and the corresponding codon from Val to Asn"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: group(250..753, 232..753)
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise C-terminal polypeptide fragments of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 253..753
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise a polypeptide fragment of FADD designated NFD-2"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 310..753
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise a polypeptide fragment of FADD designated NFD-3"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 367..753
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise polypeptide fragment of FADD designated NFD-4"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 131..504
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise an N-terminal half polypeptide fragment of FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 71..478
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise an N-terminal half polypeptide fragment of FADD designated N-FADD"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 133..501
- (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise an N-terminal half polypeptide fragment of FADD"

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cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGCGAGA CCTGGCCAGG 60  
GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA 120  
GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC 168  
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser  
1 5 10  
AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG 216  
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly  
15 20 25  
CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC 264  
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu  
30 35 40 45  
TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG 312  
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu  
50 55 60  
CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG 360  
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg  
65 70 75  
CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCG CCT GGG 408  
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly  
80 85 90  
GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG 456  
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly  
95 100 105  
AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG 504  
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys  
110 115 120 125  
ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG 552  
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val  
130 135 140  
CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA 600  
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr  
145 150 155  
GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG 648  
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val  
160 165 170  
GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG 696  
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg  
175 180 185  
AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC 744  
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser  
190 195 200 205  
GAA GCG TCC TGA TGGCCGCTG CTTTGCCTG GTGGACCACA GGCATCTACA 796  
Glu Ala Ser \*  
CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA 856  
GCCAGGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC 916

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4  
cont

TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG	976
ACACTGAGCA AGATCTTGTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG	1036
AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC	1096
GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAACG AGAGAGGTGG AGAACTGGGA	1156
TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC	1216
CCTGCAGTTG GCAGAAAGGA TGTTTGTCC CATTTCCTTG GAGGCCACCG GGACAGACCT	1276
GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGTGGG	1336
GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA	1396
GAECTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG	1456
CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCTCG	1516
CAATTCTACA GTTTCTTACT GTTTGTATC AAAATCACTA TCTTCTGAT AACAGAATTG	1576
CCAAGGCAGC GGGATCTCGT ATCTTAAAAA AGCAGTCCTC TTATTCTAA GGTAATCCTA	1636
TTAAAAA	1642

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser  
1 5 10 15

Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly  
20 25 30

Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met  
35 40 45

Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg  
50 55 60

Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp  
65 70 75 80

Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp  
85 90 95

Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp  
100 105 110

Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser  
115 120 125

Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser  
130 135 140

*a<sup>4</sup>  
Cont.*

Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His  
145 150 155 160

Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu  
165 170 175

Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala  
180 185 190

Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser  
195 200 205

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "V is replaced by asparagine(N) for the point mutant of hFADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile  
1 5 10 15

Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg  
20 25 30

Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val  
35 40 45

Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala  
50 55 60

Asp Leu Val Gln Glu Val  
65 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "I is replaced by asparagine(N) for the point mutant of rFas"

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CONT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Lys Lys Phe Ala Arg Gln His Lys Ile Pro Glu Ser Lys Ile  
1 5 10 15

Asp Glu Ile Glu His Asn Ser Pro Gln Asp Ala Ala Glu Gln Lys Ile  
20 25 30

Gln Leu Leu Gln Cys Trp Tyr Gln Ser His Gly Lys Thr Gly Ala Cys  
35 40 45

Gln Ala Leu Ile Gln Gly Leu Arg Lys Ala Asn Arg Cys Asp Ile Ala  
50 55 60

Glu Glu Ile Gln Ala Met  
65 70

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "V is replaced by asparagine(N) for the point mutant of hFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

*A4*  
*Cont.*

Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile  
1 5 10 15

Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val  
20 25 30

Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr  
35 40 45

Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala  
50 55 60

Glu Lys Ile Gln Thr Ile  
65 70

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11

(D) OTHER INFORMATION: /note= "L is replaced by asparagine for the point mutant of hTNFR-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile  
1 5 10 15

Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr  
20 25 30

Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr  
35 40 45

Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys  
50 55 60

Leu Glu Asp Ile Glu Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:7:

*a 4*  
*cont.*

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCCTGGTA CCATGCTGGG CATCTGGACC CTCCTACCTC TGGTTCTTAC GTCTGTTGCT 60  
AGATTATCGT CCAAAGACTA CAAGGACGAC GATGACAAGA GTGTTAATGC CCAAGTC 117